

PCTA9407-2(한국생명공학연구원)

<110> Korea Research Institute of Bioscience and Biotechnology

<120> A novel *Hansenula polymorpha* gene coding for alpha 1,6
mannosyltransferase and process for the production of recombinant
glycoproteins with *Hansenula polymorpha* mutant strain deficient
in the same gene

<160> 14

<170> Kopatent In 1.71

<210> 1
<211> 1351

<212> DNA
<213> *Hansenula polymorpha*

<220>
<221> CDS
<222> (10) (1293)

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                                         51

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gtg ctg aag cgc gcg cga ctc tac atg gcg acg aat cgc cg^g ctg gtg
 Val Leu Lys Arg Ala Arg Leu Tyr Met Ala Thr Asn Arg Arg Leu Val
 15 20 25 30

gtt gtt ctt gtg gtg ctg ctg tac tgg gtg gtc cag aac gtt tgg acg 147
 Val Val Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr
 35 40 45

tgg agc cct ggg acg cgc gat ttg gcc caa gtg gac gcg aag atc gag
Trp Ser Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu 195
 50 55 60

gcc gag cta aac tcg aat cta cat act ttt gga gcg cat ttg cgc cac 243
 Ala Glu Leu Asn Ser Asn Leu His Thr Phe Gly Ala His Leu Arg His
 65 70 75

tta aac ccg ctt ccg gca gag tcg gcc acc ctg cgt gaa aaa ctc acc 291
 Leu Asn Arg Leu Pro Ala Glu Ser Ala Thr Leu Arg Glu Lys Leu Thr
 80 85 90

ttc tat ttc cca tat tat cct gaa aag ccc gtg ccg aac cag atc tgg 339
 Phe Tyr Phe Pro Tyr Tyr Pro Glu Lys Pro Val Pro Asn Gln Ile Trp
 95 100 105 110

cag aca tgg aag gtc gat ctc gaa gac gac aac ttc ccc aag cag tac
 Gln Thr Trp Lys Val Asp Leu Glu Asp Asp Asn Phe Pro Lys Gln Tyr
 115 120 125

aga cggttt cag aag acg tgg gtc gag aaa aat cca gac tac gtg tac 435
Arg Arg Phe Gln Lys Thr Trp Val Glu Lys Asn Pro Asp Tyr Val Tyr
130 135 140

cac ctg att ccg gac tct gtg att gag gac ttt gtg gcg agt ttg tac
 His Leu Ile Pro Asp Ser Val Ile Glu Asp Phe Val Ala Ser Leu Tyr
 145 150 155

gct aac gtg ccg gag gtc gtc aga gct tac cag ctg ctt ccg aaa aat 531
 Ala Asn Val Pro Glu Val Val Arg Ala Tyr Gln Leu Leu Pro Lys Asn
 160 165 170

atc atg aag gcg gat ttt ttc cggtat ttggatc tac gcg cgc gga
 Ile Met Lys Ala Asp Phe Phe Arg Tyr Leu Val Ile Tyr Ala Arg Gly
 175 180 185 190

ggc acc tac tca gac atg gac acg gtg tgt tta aag ccg atc aag gac 627
 Gly Thr Tyr Ser Asp Met Asp Thr Val Cys Leu Lys Pro Ile Lys Asp
 195 200 205

tgg gcc acg ttt gat cgc gac ctg atc cac gct gcc gac aat aag gcc 675
Trp Ala Thr Phe Asp Arg Asp Leu Ile His Ala Ala Asp Asn Lys Ala

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210	215	220	
gat ctc tcc cag ata gat cca gaa gca aga acc acg cct		gtg ggg ctg	723
Asp Leu Ser Gln Ile Asp Pro Glu Ala Arg Thr Thr Pro Val Gly Leu			
225	230	235	
gtg att ggc att gag gcc gac ccg gac agg ccc gac tgg cac gag tgg			771
Val Ile Gly Ile Glu Ala Asp Pro Asp Arg Pro Asp Trp His Glu Trp			
240	245	250	
ttc tcg cgc aga ctg cag ttc tgc cag tgg acg atc cag gcg aag ccg			819
Phe Ser Arg Arg Leu Gln Phe Cys Gln Trp Thr Ile Gln Ala Lys Pro			
255	260	265	270
gga cac ccg ctg ctg cgc gag ctg atc atc cgg atc gtg gag gag acg			867
Gly His Pro Leu Leu Arg Glu Leu Ile Ile Arg Ile Val Glu Glu Thr			
275	280	285	
ttc cgc aaa cag cac atg ggc gtt ttg aaa aga gtg gaa ggc aag gac			915
Phe Arg Lys Gln His Met Gly Val Leu Lys Arg Val Glu Gly Lys Asp			
290	295	300	
tcg ggc gca gat atc atg cag tgg aca gga ccg ggg ata ttt aca gac			963
Ser Gly Ala Asp Ile Met Gln Trp Thr Gly Pro Gly Ile Phe Thr Asp			
305	310	315	
act ctg ttt gat tat ctg aac aat gtg gcg agc gac ggc aag ttg ggc			1011
Thr Leu Phe Asp Tyr Leu Asn Asn Val Ala Ser Asp Gly Lys Leu Gly			
320	325	330	
gac ggg tac ggc gtg ggg tcg ttg tat tgg cgc aag cac ggc aaa tat			1059
Asp Gly Tyr Gly Val Gly Ser Leu Tyr Trp Arg Lys His Gly Lys Tyr			
335	340	345	350
aag ctg aaa aag aca gaa att aac aag aat aac gag cca ttg cat tct			1107
Lys Leu Lys Lys Thr Glu Ile Asn Lys Asn Asn Glu Pro Leu His Ser			
355	360	365	
gag gac cag ctt atc aac tgg agg tcg ctg acc aac atg gac aag cca			1155
Glut Asp Gln Leu Ile Asn Trp Arg Ser Leu Thr Asn Met Asp Lys Pro			
370	375	380	
aag atc atg ggg gac gta atg gtg tta cca atc acg agc ttt agt ccg			1203
Lys Ile Met Gly Asp Val Met Val Leu Pro Ile Thr Ser Phe Ser Pro			
385	390	395	
aac gtg ggg cac atg ggc tca aag agc agc tca gat agg ctg gca ttt			1251
Asn Val Gly His Met Gly Ser Lys Ser Ser Asp Arg Leu Ala Phe			
400	405	410	
gtg gag cat tta ttt tct ggc agc tgg aag cca aaa aac aaa tagaaaa			1300
Val Glu His Leu Phe Ser Gly Ser Trp Lys Pro Lys Asn Lys			
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Leu Val Val Leu Leu Tyr Trp Val Val Gln Asn Val Trp Thr Trp Ser			
35 40 45			
Pro Gly Thr Arg Asp Leu Ala Gln Val Asp Ala Lys Ile Glu Ala Glu			
50 55 60			

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Leu	Asn	Ser	Asn	Leu	His	Thr	Phe	Gly	Ala	His	Leu	Arg	His	Leu	Asn
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Arg	Leu	Pro	Ala	Glu	Ser	Ala	Thr	Leu	Arg	Glu	Lys	Leu	Thr	Phe	Tyr
	85				90						95				
Phe	Pro	Tyr	Pro	Glu	Lys	Pro	Val	Pro	Asn	Gln	Ile	Trp	Gln	Thr	
	100				105						110				
Trp	Lys	Val	Asp	Leu	Glu	Asp	Asp	Asn	Phe	Pro	Lys	Gln	Tyr	Arg	Arg
	115				120						125				
Phe	Gln	Lys	Thr	Trp	Val	Glu	Lys	Asn	Pro	Asp	Tyr	Val	Tyr	His	Leu
	130				135						140				
Ile	Pro	Asp	Ser	Val	Ile	Glu	Asp	Phe	Val	Ala	Ser	Leu	Tyr	Ala	Asn
	145				150						155				160
Val	Pro	Glu	Val	Val	Arg	Ala	Tyr	Gln	Leu	Leu	Pro	Lys	Asn	Ile	Met
	165				170						175				
Lys	Ala	Asp	Phe	Phe	Arg	Tyr	Leu	Val	Ile	Tyr	Ala	Arg	Gly	Gly	Thr
	180				185						190				
Tyr	Ser	Asp	Met	Asp	Thr	Val	Cys	Leu	Lys	Pro	Ile	Lys	Asp	Trp	Ala
	195				200						205				
Thr	Phe	Asp	Arg	Asp	Leu	Ile	His	Ala	Ala	Asp	Asn	Lys	Ala	Asp	Leu
	210				215						220				
Ser	Gln	Ile	Asp	Pro	Glu	Ala	Arg	Thr	Thr	Pro	Val	Gly	Leu	Val	Ile
	225				230						235				240
Gly	Ile	Glu	Ala	Asp	Pro	Asp	Arg	Pro	Asp	Trp	His	Glu	Trp	Phe	Ser
	245				250						255				
Arg	Arg	Leu	Gln	Phe	Cys	Gln	Trp	Thr	Ile	Gln	Ala	Lys	Pro	Gly	His
	260				265						270				
Pro	Leu	Leu	Arg	Glu	Leu	Ile	Ile	Arg	Ile	Val	Glu	Glu	Thr	Phe	Arg
	275				280						285				
Lys	Gln	His	Met	Gly	Val	Leu	Lys	Arg	Val	Glu	Gly	Lys	Asp	Ser	Gly
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Ala	Asp	Ile	Met	Gln	Trp	Thr	Gly	Pro	Gly	Ile	Phe	Thr	Asp	Thr	Leu
	305				310						315				320
Phe	Asp	Tyr	Leu	Asn	Asn	Val	Ala	Ser	Asp	Gly	Lys	Leu	Gly	Asp	
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Tyr	Gly	Val	Gly	Ser	Leu	Tyr	Trp	Arg	Lys	His	Gly	Lys	Tyr	Lys	Leu
	340				345						350				
Lys	Lys	Thr	Glu	Ile	Asn	Lys	Asn	Asn	Glu	Pro	Leu	His	Ser	Glu	Asp
	355				360						365				
Gln	Leu	Ile	Asn	Trp	Arg	Ser	Leu	Thr	Asn	Met	Asp	Lys	Pro	Lys	Ile
	370				375						380				
Met	Gly	Asp	Val	Met	Val	Leu	Pro	Ile	Thr	Ser	Phe	Ser	Pro	Asn	Val
	385				390						395				400
Gly	His	Met	Gly	Ser	Lys	Ser	Ser	Ser	Asp	Arg	Leu	Ala	Phe	Val	Glu
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39

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PCTA9407-2(한국생명공학연구원)

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<210> 12
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<210> 13
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Aspergillus saitoi

<400> 13
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33

<210> 14
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<212> DNA
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Aspergillus saitoi

<400> 14

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caccggcac	69